

# SEQ ID NO 1

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 02:59:20 ; Search time 5492.57 Seconds  
(without alignments)  
10812.700 Million cell updates/sec

Title: US-09-801-267-1  
Perfect score: 2838  
Sequence: 1 ggttttccacgtttgcntg.....aaaaaaaaaaaaaggcgaa 2838

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pat:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_sts:

```

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2788.2	98.2	2838	6	AX249742	AX249742 Sequence
2	2397.6	84.5	2495	9	AK057079	AK057079 Homo sapi
3	2287.6	80.6	2634	6	AX287089	AX287089 Sequence
4	2280.8	80.4	250681	9	AP004282	AP004282 Homo sapi
5	2093.8	73.8	2555	9	AF155661	AF155661 Homo sapi
6	1632.6	57.5	1725	6	AX180883	AX180883 Sequence
7	1632	57.5	1779	6	AX277696	AX277696 Sequence
8	1611	56.8	1611	6	AX249744	AX249744 Sequence
9	1519.8	53.6	2295	10	AF062740	AF062740 Rattus no
10	1486.4	52.4	1900	4	BOVPHOS	L18966 Bos taurus
11	1091.8	38.5	2598	9	AK022057	AK022057 Homo sapi
12	495.2	17.4	66671	2	AC101372	AC101372 Mus muscu
c 13	450.6	15.9	66671	2	AC101372	AC101372 Mus muscu
14	426	15.0	1750	10	AF062741	AF062741 Rattus no
15	405.6	14.3	1924	6	AX287088	AX287088 Sequence
16	405.6	14.3	3830	9	AB037769	AB037769 Homo sapi
17	405.6	14.3	206102	9	AC027131	AC027131 Homo sapi
18	364.6	12.8	1567	5	AF294839	AF294839 Danio rer
19	342.8	12.1	357	6	AX255966	AX255966 Sequence
c 20	331.6	11.7	66199	2	AC101398	AC101398 Mus muscu
21	229.8	8.1	1716	6	AX179297	AX179297 Sequence
22	222.4	7.8	2535	6	AX179295	AX179295 Sequence
23	220.6	7.8	183865	9	AC009084	AC009084 Homo sapi
24	210	7.4	1909	6	AX179289	AX179289 Sequence
25	208	7.3	1948	6	AX262513	AX262513 Sequence
c 26	199.2	7.0	289	11	G05827	G05827 human STS W
c 27	196.6	6.9	91605	2	AC096087	AC096087 Rattus no
28	192.2	6.8	1503	9	AK000576	AK000576 Homo sapi
29	192.2	6.8	1683	9	AK026847	AK026847 Homo sapi
30	192.2	6.8	1755	9	AK000572	AK000572 Homo sapi
31	190	6.7	1699	6	AX179293	AX179293 Sequence
32	187.6	6.6	5150	9	AB056777	AB056777 Macaca fa
33	176.2	6.2	3392	12	AB009864	AB009864 Expressio
34	171.6	6.0	4951	6	AR073576	AR073576 Sequence
35	168.4	5.9	2286	9	AK027005	AK027005 Homo sapi
36	154	5.4	4026	6	AR098191	AR098191 Sequence
37	154	5.4	4026	6	BD009730	BD009730 Tissue sp
38	152.6	5.4	3639	12	SYNPKA1	D13749 Plasmid pKA
39	150	5.3	4234	12	AB007632	AB007632 Signal se
40	149.2	5.3	6311	12	AF326321	AF326321 Shuttle v
41	148.4	5.2	2248	9	AK026975	AK026975 Homo sapi

42	148.4	5.2	2821	6	AX195202	AX195202 Sequence
43	148.4	5.2	2833	6	AX195203	AX195203 Sequence
44	148.4	5.2	2845	6	AX195204	AX195204 Sequence
45	148.4	5.2	3796	6	E49323	E49323 Infectious

OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 04:39:06 ; Search time 483.19 Seconds  
(without alignments)  
10084.238 Million cell updates/sec

Title: US-09-801-267-1  
Perfect score: 2838  
Sequence: 1 gttttccacgtttgcntg.....aaaaaaaaaaaaaggcgaa 2838

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_032802:  
1: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT:\*2: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:\*3: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:\*4: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT:\*5: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT:\*6: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT:\*7: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:\*8: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT:\*9: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:\*10: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT:\*11: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT:\*12: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT:\*13: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1992.DAT:\*14: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT:\*15: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT:\*16: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT:\*17: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT:\*18: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:\*19: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:\*20: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:\*21: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:\*22: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:\*23: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:\*24: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result %  
Query

No.	Score	Match	Length	DB	ID	Description
1	2788.2	98.2	2838	22	AAD15455	Human 26583 serine
2	2287.6	80.6	2634	24	AAD23607	Human protein phos
3	1734.8	61.1	4466	22	AAS31175	Human diagnostic a
4	1632.6	57.5	1725	22	AAD09500	Human SGP040 phosp
5	1632	57.5	1779	24	AAI64180	Human pyruvate deh
6	1577.8	55.6	1935	22	AAC91346	Human polynucleoti
7	1091.8	38.5	2598	22	AAH17300	Human cDNA sequenc
8	686	24.2	711	21	AAC75877	Human ORFX ORF1432
9	637.4	22.5	642	22	AAH04418	Human cDNA clone (
10	544	19.2	560	22	AAS31351	Human cDNA encodin
11	463.8	16.3	481	22	AAS31456	Human cDNA encodin
12	405.6	14.3	1924	24	AAD23606	Human protein phos
c 13	358.4	12.6	372	22	AAL13831	Human breast cance
c 14	358.4	12.6	386	22	AAL13615	Human breast cance
c 15	355.6	12.5	775	22	AAI94857	Human neuroblastom
c 16	348.4	12.3	352	22	AAL22484	Human breast cance
c 17	348.4	12.3	352	22	AAL22485	Human breast cance
c 18	346.8	12.2	352	22	AAL22697	Human breast cance
c 19	342.8	12.1	357	22	AAS56493	Human cDNA for an
c 20	310.4	10.9	316	22	AAL13616	Human breast cance
21	229.8	8.1	1716	22	AAH25135	Nucleotide sequenc
22	222.4	7.8	2535	22	AAH25134	Nucleotide sequenc
23	219.4	7.7	494	21	AAZ80336	Human colon cancer
24	210	7.4	1909	22	AAH25131	Nucleotide sequenc
25	208	7.3	1948	22	AAI66824	Human protein kina
c 26	194	6.8	802	22	AAI96456	Human neuroblastom
c 27	193	6.8	833	22	AAI97575	Human neuroblastom
c 28	192.8	6.8	747	22	AAI97540	Human neuroblastom
c 29	192.8	6.8	815	22	AAI95997	Human neuroblastom
c 30	192.2	6.8	706	22	AAI97826	Human neuroblastom
c 31	192.2	6.8	715	22	AAI97882	Human neuroblastom
c 32	192.2	6.8	737	22	AAI97535	Human neuroblastom
c 33	192.2	6.8	751	22	AAI97536	Human neuroblastom
c 34	192.2	6.8	759	22	AAI97550	Human neuroblastom
c 35	192.2	6.8	768	22	AAI96393	Human neuroblastom
c 36	192.2	6.8	775	22	AAI97555	Human neuroblastom
c 37	192.2	6.8	790	22	AAI96496	Human neuroblastom
c 38	192.2	6.8	838	22	AAI97591	Human neuroblastom
c 39	192.2	6.8	915	22	AAI97906	Human neuroblastom
c 40	192.2	6.8	942	22	AAI97728	Human neuroblastom
c 41	191.8	6.8	727	22	AAI96563	Human neuroblastom
c 42	191.2	6.7	761	22	AAI97544	Human neuroblastom
c 43	190.8	6.7	835	22	AAI97581	Human neuroblastom
44	190	6.7	1699	22	AAH25133	Nucleotide sequenc
c 45	188.4	6.6	776	22	AAI96362	Human neuroblastom

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 03:07:20 ; Search time 95.42 Seconds  
(without alignments)  
7305.679 Million cell updates/sec

Title: US-09-801-267-1  
Perfect score: 2838

Sequence: 1 ggtttccacgtttgcntg.....aaaaaaaaaaaaaggcgaa 2838

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Query				Description
	Score	Match	Length	DB	
1	219.4	7.7	494	4	US-09-328-111-420 Sequence 420, Appl
2	171.6	6.0	4951	2	US-08-752-307B-1 Sequence 1, Appli
3	154	5.4	4026	3	US-08-801-092-19 Sequence 19, Appl
4	151.4	5.3	7287	2	US-08-659-206A-1 Sequence 1, Appli
5	148.4	5.2	6253	3	US-08-893-327-15 Sequence 15, Appl
6	148.4	5.2	6280	3	US-08-893-327-17 Sequence 17, Appl
7	148.4	5.2	6280	3	US-08-893-327-19 Sequence 19, Appl
8	148.4	5.2	6295	2	US-08-659-206A-4 Sequence 4, Appli
9	148.4	5.2	7852	3	US-08-836-022A-2 Sequence 2, Appli
10	148.4	5.2	7852	4	US-09-427-048A-2 Sequence 2, Appli
11	148.4	5.2	7892	2	US-07-916-098A-40 Sequence 40, Appl
c 12	148.4	5.2	7897	3	US-08-836-022A-1 Sequence 1, Appli

c	13	148.4	5.2	7897	4	US-09-427-048A-1	Sequence 1, Appli
	14	148.4	5.2	8236	1	US-08-461-837-1	Sequence 1, Appli
	15	148.4	5.2	8236	3	US-08-973-223-1	Sequence 1, Appli
	16	148.4	5.2	8236	4	US-09-347-060-1	Sequence 1, Appli
	17	148.4	5.2	8236	5	PCT-US96-09495-1	Sequence 1, Appli
	18	148.4	5.2	8509	1	US-08-462-014-1	Sequence 1, Appli
	19	148.4	5.2	8509	4	US-08-973-334-4	Sequence 4, Appli
	20	148.4	5.2	8509	4	US-09-563-869A-4	Sequence 4, Appli
	21	148.4	5.2	10398	2	US-08-331-384-1	Sequence 1, Appli
	22	148.4	5.2	10398	2	US-08-708-188-1	Sequence 1, Appli
	23	148.4	5.2	10398	2	US-08-836-087-1	Sequence 1, Appli
	24	148.4	5.2	10398	4	US-09-246-320-1	Sequence 1, Appli
	25	148.4	5.2	10398	4	US-09-242-743-1	Sequence 1, Appli
c	26	148.4	5.2	19307	3	US-08-836-022A-10	Sequence 10, Appli
c	27	148.4	5.2	19307	4	US-09-427-048A-10	Sequence 10, Appli
	28	105.4	3.7	160	4	US-09-116-032-25	Sequence 25, Appli
	29	104.8	3.7	4249	3	US-08-801-092-33	Sequence 33, Appli
	30	104.2	3.7	1028	1	US-08-029-328-1	Sequence 1, Appli
	31	104	3.7	5620	2	US-08-793-170-21	Sequence 21, Appli
	32	104	3.7	5620	3	US-08-892-873-21	Sequence 21, Appli
	33	104	3.7	5620	4	US-09-334-765A-21	Sequence 21, Appli
	34	104	3.7	5620	4	US-09-356-575E-21	Sequence 21, Appli
	35	104	3.7	5620	4	US-09-333-820-21	Sequence 21, Appli
	36	89.2	3.1	5183	3	US-09-039-555B-18	Sequence 18, Appli
c	37	89.2	3.1	5243	2	US-08-414-335-2	Sequence 2, Appli
	38	82.6	2.9	6124	4	US-08-213-419B-3	Sequence 3, Appli
	39	80	2.8	80	4	US-09-116-032-29	Sequence 29, Appli
	40	73.4	2.6	7218	1	US-08-232-463-14	Sequence 14, Appli
c	41	70	2.5	5852	1	US-07-867-106-2	Sequence 2, Appli
	42	68.8	2.4	4880	3	US-09-031-563-1	Sequence 1, Appli
	43	68.8	2.4	5125	3	US-09-031-563-4	Sequence 4, Appli
	44	68.2	2.4	1074	3	US-09-248-335-67	Sequence 67, Appli
	45	68.2	2.4	2481	2	US-08-630-118A-1	Sequence 1, Appli

OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 02:56:45 ; Search time 3497.84 Seconds  
(without alignments)  
10950.861 Million cell updates/sec

Title: US-09-801-267-1

Perfect score: 2838

Sequence: 1 ggttttccacgtttgcntg.....aaaaaaaaaaaaaggcgaa 2838

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_gss:\*

13: em\_gss\_hum:\*

14: em\_gss\_inv:\*

15: em\_gss\_pln:\*

16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	637.4	22.5	642	9	AU120803	AU120803 AU120803
2	634.6	22.4	642	10	BG703862	BG703862 602686908
3	606.8	21.4	631	9	AV705571	AV705571 AV705571
4	606.8	21.4	725	9	AV710801	AV710801 AV710801
5	605.4	21.3	649	9	AV706533	AV706533 AV706533

6	588	20.7	688	10	BI460642	BI460642	603201289
7	562.4	19.8	608	10	BG720546	BG720546	602691803
8	554.4	19.5	723	9	AU136538	AU136538	AU136538
9	542	19.1	651	9	BB625845	BB625845	BB625845
10	488.6	17.2	640	9	BB617574	BB617574	BB617574
11	477	16.8	571	9	AW060691	AW060691	UI-M-BH1-
c 12	474	16.7	600	9	AI767779	AI767779	wi96d09.x
c 13	464.8	16.4	637	9	BB623274	BB623274	BB623274
c 14	460.2	16.2	549	9	BE222048	BE222048	hu05b08.x
c 15	455	16.0	533	9	AI593115	AI593115	vr31a07.y
c 16	451	15.9	543	9	AI052520	AI052520	oz27f03.x
c 17	415	14.6	522	9	AA637163	AA637163	vr31a07.r
c 18	403.2	14.2	492	9	BE048495	BE048495	hr49g02.x
19	400.6	14.1	590	10	BG088579	BG088579	H3155A02-
c 20	394.8	13.9	490	9	AW467157	AW467157	ha35c05.x
21	378	13.3	583	9	BB611000	BB611000	BB611000
22	374.6	13.2	469	9	AI505570	AI505570	vr31a07.x
23	373.4	13.2	703	9	AW964337	AW964337	EST376410
c 24	373	13.1	373	9	AI024308	AI024308	ov67f02.x
25	364.2	12.8	479	10	H09827	H09827	ym01a02.r1
26	359	12.6	443	10	H10695	H10695	ym07h07.r1
27	345.4	12.2	468	10	BG795101	BG795101	UTSW_SM29
28	343.6	12.1	462	10	BG796457	BG796457	UTSW_SM43
c 29	335.8	11.8	543	10	BG038714	BG038714	dd93f05.x
c 30	335.2	11.8	424	9	AI378372	AI378372	tc78c10.x
31	334	11.8	464	9	BB862687	BB862687	BB862687
c 32	328.6	11.6	401	9	BE161595	BE161595	MR3-HT044
33	326.4	11.5	368	10	BF798554	BF798554	CM0-CI006
c 34	320.6	11.3	412	9	AA628776	AA628776	af42c02.s
35	320	11.3	320	10	F05984	F05984	HSCOTA041 n
36	314.8	11.1	472	9	BB857598	BB857598	BB857598
37	314	11.1	376	10	T08925	T08925	EST06817 In
38	303.6	10.7	446	9	AW520836	AW520836	UI-R-BJ0p
39	303.4	10.7	463	9	BB860561	BB860561	BB860561
c 40	301	10.6	417	9	AI571213	AI571213	tn43e03.x
c 41	297.2	10.5	386	9	AI262149	AI262149	qz28e06.x
42	295.2	10.4	412	9	BE103025	BE103025	UI-R-BT1-
c 43	293.2	10.3	382	9	AI014504	AI014504	ou32e12.x
c 44	290.6	10.2	382	9	AI265979	AI265979	qm46b07.x
45	289	10.2	307	9	AW606530	AW606530	MR2-HT038

# SEQ ID NO 2

Run on: August 17, 2002, 07:13:31 ; Search time 58.15 Seconds  
(without alignments)  
1025.737 Million cell updates/sec

Title: US-09-801-267-2  
Perfect score: 2854

Sequence: 1 MPAPTQLFFPLIRNCELSRI.....ITIIVVQFNSHVVGAYQNQE 537

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*

4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*

5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*

6: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*

7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*

8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*

9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*

10: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:\*

11: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*

12: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:\*

13: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*

14: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:\*

15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:\*

16: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:\*

17: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:\*

18: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:\*

19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:\*

20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*

21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*

22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	2854	100.0	537	22	AAE09249		Human 26583 serine
2	2767	97.0	574	22	AAE04842		Human SGP040 phosph

3	979	34.3	237	21	AAB41668	Human ORFX ORF1432
4	838.5	29.4	475	22	ABB59189	Drosophila melanog
5	791	27.7	186	22	AAU19780	Human novel extrac
6	639	22.4	160	22	AAU19885	Human novel extrac
7	590	20.7	114	22	AAB95012	Human protein sequ
8	563	19.7	135	22	AAU19604	Human diagnostic a
9	366.5	12.8	194	22	AAM80161	Human protein SEQ
10	296	10.4	397	22	AAB80624	Environmental stre
11	274	9.6	379	21	AAG36375	Arabidopsis thalia
12	274	9.6	384	21	AAG36374	Arabidopsis thalia
13	273	9.6	324	21	AAG36376	Arabidopsis thalia
14	266.5	9.3	385	21	AAG13464	Arabidopsis thalia
15	265.5	9.3	336	21	AAG13465	Arabidopsis thalia
16	258.5	9.1	380	21	AAG24234	Arabidopsis thalia
17	258.5	9.1	380	21	AAG39915	Arabidopsis thalia
18	258.5	9.1	380	21	AAY77934	A. thaliana enviro
19	258	9.0	113	22	AAM79177	Human protein SEQ
20	247	8.7	465	21	AAG14228	Arabidopsis thalia
21	247	8.7	521	21	AAG14227	Arabidopsis thalia
22	247	8.7	662	21	AAG14226	Arabidopsis thalia
23	242.5	8.5	355	21	AAG43887	Arabidopsis thalia
24	242.5	8.5	357	21	AAG43237	Arabidopsis thalia
25	240.5	8.4	378	21	AAG13816	Arabidopsis thalia
26	240.5	8.4	386	21	AAG13815	Arabidopsis thalia
27	240.5	8.4	393	21	AAG13814	Arabidopsis thalia
28	240	8.4	270	21	AAG13466	Arabidopsis thalia
29	239	8.4	384	21	AAG28394	Arabidopsis thalia
30	239	8.4	493	21	AAG28393	Arabidopsis thalia
31	238	8.3	384	21	AAG21784	Arabidopsis thalia
32	238	8.3	384	21	AAG49572	Arabidopsis thalia
33	238	8.3	493	21	AAG21783	Arabidopsis thalia
34	238	8.3	493	21	AAG49571	Arabidopsis thalia
35	236.5	8.3	438	22	AAB82980	Trichoderma reesei
36	231.5	8.1	329	21	AAG43238	Arabidopsis thalia
37	229.5	8.0	327	21	AAG43888	Arabidopsis thalia
38	228.5	8.0	322	21	AAG43239	Arabidopsis thalia
39	228.5	8.0	360	21	AAG28395	Arabidopsis thalia
40	227.5	8.0	360	21	AAG21785	Arabidopsis thalia
41	227.5	8.0	360	21	AAG49573	Arabidopsis thalia
42	226.5	7.9	320	21	AAG43889	Arabidopsis thalia
43	221	7.7	360	21	AAG16902	Arabidopsis thalia
44	218.5	7.7	267	21	AAG24236	Arabidopsis thalia
45	218.5	7.7	267	21	AAG39917	Arabidopsis thalia

Search completed: August 17, 2002, 09:08:32  
Job time: 6901 sec

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OM protein - protein search, using sw model

Run on: August 17, 2002, 07:21:01 ; Search time 24.36 Seconds  
(without alignments)  
538.446 Million cell updates/sec

Title: US-09-801-267-2  
Perfect score: 2854  
Sequence: 1 MPAPTQLFFPLIRNCELSRI.....ITIIVVQFNSHVVGAYQNQE 537

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	%	Match	Length	DB	ID	Description
1	209	7.3	392	4	US-09-013-881-2		Sequence 2, Appli
2	188	6.6	281	2	US-08-822-701-9		Sequence 9, Appli
3	188	6.6	281	3	US-08-935-855-9		Sequence 9, Appli
4	175.5	6.1	546	3	US-08-935-855-20		Sequence 20, Appl
5	173.5	6.1	392	2	US-08-822-701-2		Sequence 2, Appli
6	173.5	6.1	392	3	US-08-935-855-2		Sequence 2, Appli
7	173.5	6.1	542	3	US-08-935-855-22		Sequence 22, Appl
8	172	6.0	309	2	US-08-822-701-7		Sequence 7, Appli
9	172	6.0	309	3	US-08-935-855-7		Sequence 7, Appli

10	171.5	6.0	390	2	US-08-873-093-3	Sequence 3, Appli
11	169.5	5.9	478	2	US-08-873-093-1	Sequence 1, Appli
12	169.5	5.9	478	2	US-08-873-093-4	Sequence 4, Appli
13	154	5.4	504	2	US-08-752-891-6	Sequence 6, Appli
14	154	5.4	504	2	US-09-144-178-6	Sequence 6, Appli
15	154	5.4	504	4	US-09-406-854-6	Sequence 6, Appli
16	148	5.2	504	2	US-08-752-891-2	Sequence 2, Appli
17	148	5.2	504	2	US-09-144-178-2	Sequence 2, Appli
18	148	5.2	504	4	US-09-406-854-2	Sequence 2, Appli
19	137.5	4.8	306	2	US-08-822-701-8	Sequence 8, Appli
20	137.5	4.8	306	3	US-08-935-855-8	Sequence 8, Appli
21	133	4.7	314	2	US-08-822-701-10	Sequence 10, Appli
22	133	4.7	314	3	US-08-935-855-10	Sequence 10, Appli
23	112.5	3.9	465	4	US-09-346-408-6	Sequence 6, Appli
24	111.5	3.9	752	1	US-08-309-512-8	Sequence 8, Appli
25	111.5	3.9	752	5	PCT-US92-08756A-8	Sequence 8, Appli
26	103.5	3.6	896	1	US-08-095-737-2	Sequence 2, Appli
27	103.5	3.6	896	1	US-08-480-145-2	Sequence 2, Appli
28	103.5	3.6	896	2	US-08-477-389-2	Sequence 2, Appli
29	100.5	3.5	528	3	US-08-747-221B-37	Sequence 37, Appli
30	100.5	3.5	528	4	US-09-005-051-37	Sequence 37, Appli
31	97	3.4	997	1	US-08-232-540-1	Sequence 1, Appli
32	97	3.4	997	1	US-08-428-949A-1	Sequence 1, Appli
33	97	3.4	997	1	US-08-428-948A-1	Sequence 1, Appli
34	97	3.4	997	2	US-08-428-946-1	Sequence 1, Appli
35	97	3.4	997	5	PCT-US95-04656-1	Sequence 1, Appli
36	97	3.4	998	1	US-08-233-008A-6	Sequence 6, Appli
37	97	3.4	1021	1	US-08-233-008A-2	Sequence 2, Appli
38	95.5	3.3	937	3	US-09-005-180A-4	Sequence 4, Appli
39	95.5	3.3	1455	2	US-08-726-012B-2	Sequence 2, Appli
40	94	3.3	510	1	US-08-097-829-2	Sequence 2, Appli
41	94	3.3	510	1	US-08-577-403-2	Sequence 2, Appli
42	93	3.3	2432	4	US-09-074-658-15	Sequence 15, Appli
43	92.5	3.2	860	1	US-08-117-362-3	Sequence 3, Appli
44	92.5	3.2	860	1	US-08-486-924-3	Sequence 3, Appli
45	92.5	3.2	2439	4	US-09-074-658-11	Sequence 11, Appli

Search completed: August 17, 2002, 09:10:22  
Job time: 6561 sec

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OM protein - protein search, using sw model

Run on: August 17, 2002, 07:20:06 ; Search time 42.44 Seconds  
(without alignments)  
1215.833 Million cell updates/sec

Title: US-09-801-267-2

Perfect score: 2854

Sequence: 1 MPAPTQLFFPLIRNCELSRI.....ITIIVVQFNSHVVGAYQNQE 537

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_71:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	2798	98.0	538	2	A48692 [pyruvate dehydrog
2	507.5	17.8	622	2	T49426 Type 2C Protein Ph
3	457.5	16.0	350	2	T37511 probable phosphopr
4	435	15.2	572	2	S61650 hypothetical prote
5	303.5	10.6	674	2	T48261 hypothetical prote
6	300.5	10.5	361	2	T48297 protein phosphatas
7	292.5	10.2	395	2	T05680 hypothetical prote
8	278	9.7	379	2	T45768 protein phosphatas
9	271	9.5	409	2	T47644 protein phosphatas
10	268	9.4	309	2	T51101 protein phosphatas
11	259	9.1	396	2	T51100 protein phosphatas

12	258.5	9.1	380	2	T05220	hypothetical prote
13	256.5	9.0	654	2	B84690	hypothetical prote
14	247	8.7	662	2	G86210	hypothetical prote
15	242.5	8.5	355	2	H84643	probable protein p
16	242.5	8.5	357	2	T06308	protein phosphatas
17	224.5	7.9	511	2	F96752	protein phosphatas
18	217.5	7.6	491	2	B86297	F309.3 protein - A
19	211	7.4	464	2	H96700	protein F12A21.5 [
20	211	7.4	514	2	D84584	probable protein p
21	210.5	7.4	503	2	T00901	hypothetical prote
22	209.5	7.3	442	2	B86209	protein F22G5.22 [
23	209	7.3	356	2	T25181	hypothetical prote
24	207	7.3	348	2	E88434	protein T23F11.1 [
25	199.5	7.0	370	2	S54297	protein phosphatas
26	196.5	6.9	381	2	T09640	protein phosphatas
27	196.5	6.9	814	2	T02195	hypothetical prote
28	196	6.9	393	2	S48288	probable phosphopr
29	194.5	6.8	388	2	C85323	protein phosphatas
30	194	6.8	743	2	E84767	hypothetical prote
31	192.5	6.7	386	2	T09019	phosphoprotein pho
32	192	6.7	300	2	A55804	phosphoprotein pho
33	192	6.7	390	2	C84826	protein phosphatas
34	192	6.7	414	2	S62462	protein phosphatas
35	191	6.7	383	2	T48018	hypothetical prote
36	191	6.7	434	2	T04263	phosphoprotein pho
37	190	6.7	533	2	E96827	protein F20B17.6 [
38	189.5	6.6	380	2	E84748	probable protein p
39	188.5	6.6	405	2	F86206	hypothetical prote
40	188.5	6.6	491	2	T16354	hypothetical prote
41	188	6.6	281	2	S41854	phosphoprotein pho
42	185.5	6.5	359	2	T52337	phosphoprotein pho
43	185	6.5	348	2	T50783	protein phosphatas
44	183.5	6.4	268	2	T04610	protein phosphatas
45	181	6.3	320	2	T48191	hypothetical prote

Search completed: August 17, 2002, 09:09:37  
Job time: 6571 sec

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OM protein - protein search, using sw model

Run on: August 17, 2002, 09:09:41 ; Search time 23.95 Seconds  
(without alignments)  
868.159 Million cell updates/sec

Title: US-09-801-267-2  
Perfect score: 2854  
Sequence: 1 MPAPQLFFPLIRNCELSRI.....ITIIVVQFNSHVVGAYQNQE 537

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	2804	98.2	538	1 PDP1_RAT	O88483 rattus norv
2	2798	98.0	538	1 PDP1_BOVIN	P35816 bos taurus
3	2767	97.0	538	1 PDP1_HUMAN	Q9p0j1 homo sapien
4	1322.5	46.3	530	1 PDP2_RAT	O88484 rattus norv
5	1313	46.0	529	1 PDP2_HUMAN	Q9p2j9 homo sapien
6	209	7.3	356	1 P2C2_CAEEL	P49596 caenorhabdi
7	200	7.0	605	1 P2CD_HUMAN	O15297 homo sapien
8	199.5	7.0	370	1 P2C2_SCHPO	Q09172 schizosacch
9	196	6.9	393	1 YBX5_YEAST	P38089 saccharomyc
10	194.5	6.8	388	1 P2C3_ARATH	P49599 arabidopsis
11	192	6.7	300	1 P2C_PARTE	P49444 paramecium
12	192	6.7	414	1 P2C3_SCHPO	Q09173 schizosacch
13	191	6.7	434	1 P2C1_ARATH	P49597 arabidopsis
14	188.5	6.6	491	1 P2C1_CAEEL	P49595 caenorhabdi
15	188	6.6	281	1 P2C1_YEAST	P35182 saccharomyc

16	188	6.6	423	1	P2C2_ARATH	O04719 arabidopsis
17	180.5	6.3	598	1	P2CD_MOUSE	Q9qz67 mus musculu
18	177	6.2	399	1	P2C4_ARATH	P49598 arabidopsis
19	176.5	6.2	387	1	P2CB_BOVIN	O62830 bos taurus
20	175.5	6.1	546	1	P2CG_HUMAN	O15355 homo sapien
21	173.5	6.1	542	1	P2CG_MOUSE	Q61074 mus musculu
22	171.5	6.0	390	1	P2CB_RAT	P35815 rattus norv
23	169.5	5.9	479	1	P2CB_HUMAN	O75688 homo sapien
24	167.5	5.9	390	1	P2CB_MOUSE	P36993 mus musculu
25	164	5.7	464	1	P2C2 YEAST	P39966 saccharomyc
26	164	5.7	543	1	P2CG_BOVIN	P79126 bos taurus
27	162	5.7	468	1	P2C3 YEAST	P34221 saccharomyc
28	161.5	5.7	2493	1	CYAA_USTMA	P49606 ustilago ma
29	160.5	5.6	1839	1	CYAA_SACKL	P23466 saccharomyc
30	153.5	5.4	383	1	P2C4_SCHPO	O14156 schizosacch
31	148.5	5.2	347	1	P2C1_SCHPO	P40371 schizosacch
32	148	5.2	504	1	TAB1_HUMAN	Q15750 homo sapien
33	147	5.2	2026	1	CYAA YEAST	P08678 saccharomyc
34	144.5	5.1	2145	1	CYAA PODAN	Q01513 podospora a
35	142	5.0	454	1	P2CH_HUMAN	P49593 homo sapien
36	139.5	4.9	382	1	P2CA_BOVIN	O62829 bos taurus
37	137.5	4.8	382	1	P2CA_HUMAN	P35813 homo sapien
38	137.5	4.8	382	1	P2CA_RABIT	P35814 oryctolagus
39	137.5	4.8	382	1	P2CA_RAT	P20650 rattus norv
40	136.5	4.8	382	1	P2CA_MOUSE	P49443 mus musculu
41	135	4.7	435	1	YCW9 YEAST	P25646 saccharomyc
42	134.5	4.7	2300	1	CYAA_NEUCR	Q01631 neurospora
43	133	4.7	406	1	P2C LEICH	P36982 leishmania
44	127.5	4.5	1692	1	CYAA_SCHPO	P14605 schizosacch
45	119.5	4.2	449	1	FEM2 CAEEL	P49594 caenorhabdi

OM protein - protein search, using sw model

Run on: August 17, 2002, 09:08:36 ; Search time 67.07 Seconds  
(without alignments)  
1385.094 Million cell updates/sec

Title: US-09-801-267-2  
Perfect score: 2854  
Sequence: 1 MPAPTQLFFPLIRNCELSRI.....ITIIVVQFNSHVVGAYQNQE 537

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*

1: sp\_archea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rat:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacterioplasm:\*

17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1284.5	45.0	514	13	Q9DF59	Q9df59 brachydanio
2	838.5	29.4	475	5	Q9W3Q1	Q9w3ql drosophila
3	716.5	25.1	451	5	Q9N4M0	Q9n4m0 caenorhabdi
4	507.5	17.8	594	3	Q9P6E2	Q9p6e2 neurospora
5	480.5	16.8	507	3	O14189	O14189 schizosacch

6	435	15.2	572	3	Q12511	Q12511	saccharomyc
7	303.5	10.6	674	10	Q9LZ86	Q9lz86	arabidopsis
8	300.5	10.5	361	10	Q9LZ09	Q9lz09	arabidopsis
9	292.5	10.2	395	10	Q9SZN2	Q9szn2	arabidopsis
10	284.5	10.0	376	10	Q9C7B3	Q9c7b3	arabidopsis
11	284.5	10.0	385	10	Q9LHJ9	Q9lhj9	arabidopsis
12	278	9.7	379	10	Q9SD12	Q9sd12	arabidopsis
13	274	9.6	379	10	Q9LSN8	Q9lsn8	arabidopsis
14	272	9.5	397	10	Q9M3V0	Q9m3v0	fagus sylva
15	271	9.5	384	10	Q94CL8	Q94cl8	arabidopsis
16	271	9.5	409	10	Q9M2W1	Q9m2w1	arabidopsis
17	270	9.5	388	10	Q9AV42	Q9av42	oryza sativ
18	268	9.4	309	10	Q82479	Q82479	mesembryant
19	266.5	9.3	385	10	Q9FKX4	Q9fkx4	arabidopsis
20	263.5	9.2	650	10	Q9SR24	Q9sr24	arabidopsis
21	261	9.1	337	10	Q9XGZ9	Q9xgz9	arabidopsis
22	259	9.1	396	10	Q9ZSQ7	Q9zsq7	mesembryant
23	258.5	9.1	380	10	Q81760	Q81760	arabidopsis
24	256.5	9.0	362	10	Q9ZPL9	Q9zpl9	lotus japon
25	256.5	9.0	654	10	Q9ZV25	Q9zv25	arabidopsis
26	256	9.0	294	10	Q949Y7	Q949y7	arabidopsis
27	247	8.7	662	10	Q9LQN6	Q9lqn6	arabidopsis
28	246.5	8.6	386	10	Q9FG32	Q9fg32	arabidopsis
29	243.5	8.5	366	10	Q9FQY2	Q9fqty2	zea mays (m
30	242.5	8.5	355	10	Q81716	Q81716	arabidopsis
31	242.5	8.5	357	10	Q9SZ53	Q9sz53	arabidopsis
32	241	8.4	380	10	Q94H98	Q94h98	oryza sativ
33	238	8.3	493	10	Q9LUS8	Q9lus8	arabidopsis
34	227	8.0	380	10	Q82468	Q82468	mesembryant
35	226	7.9	351	10	Q9LRZ4	Q9lrz4	arabidopsis
36	224.5	7.9	511	10	Q81709	Q81709	arabidopsis
37	224.5	7.9	511	10	Q9CAJ0	Q9caj0	arabidopsis
38	222	7.8	322	5	Q9U5F4	Q9u5f4	entamoeba h
39	217.5	7.6	491	10	Q9SA22	Q9sa22	arabidopsis
40	217	7.6	614	5	Q9VR62	Q9vr62	drosophila
41	214	7.5	416	10	Q9FLI3	Q9fli3	arabidopsis
42	214	7.5	448	10	Q9FG61	Q9fg61	arabidopsis
43	212.5	7.4	380	10	Q9FYN7	Q9fyn7	oryza sativ
44	212.5	7.4	396	10	Q9LP12	Q9lp12	arabidopsis
45	211	7.4	464	10	Q9FXE4	Q9fxe4	arabidopsis

# nucleic acid encoding Seq ID 2

OM of: US-09-801-267-2 to: GenEmbl:\* out\_format : pfs

Date: Aug 17, 2002 10:18 AM

About: Results were produced by the GenCore software, version 4.5,  
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Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlh
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Q=/cgn2_1/USPTO_spool/US09801267/runat_15082002_100802_5407/app_query.fasta_1.60
1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09801267 @CGN1_1_4493
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1
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Search information block:

Query: US-09-801-267-2  
Query length: 537  
Database: GenEmbl:\*

Database sequences: 1797656  
Database length: 1873333701  
Search time (sec): 2026.990000

score\_list:

Sequence	Strd	Orig	ZScore	EScore	Len	! Documentation ..
gb_pat:AX249744	+	2854.00	4164.34	1.4e-223	1611	! AX249744 Sequence 3
from Patent WO0166765.	9/2001					
gb_pat:AX287089	+	2854.00	4159.15	2.6e-223	2634	! AX287089 Sequence 9
from Patent WO0181590.	11/2001					
gb_pat:AX249742	+	2854.00	4158.37	2.9e-223	2838	! AX249742 Sequence 1
from Patent WO0166765.	9/2001					
gb_pr:AP004282	+	2854.00	4111.11	1.2e-220	250681	! AP004282 Homo
sapiens genomic DNA, chromosome 8q23, clone:						
KB1165G2.	12/2001					
gb_pr:AK057079	+	2845.00	4146.54	1.3e-222	2495	! AK057079 Homo sapiens
cDNA FLJ32517 fis, clone SMINT1000117, highly similar to [PYR						
gb_pat:AX277696	+	2825.00	4120.82	3.6e-221	1779	! AX277696 Sequence 1
from Patent WO0177339.	11/2001					
gb_ro:AF062740	+	2804.00	4087.37	2.6e-219	2295	! AF062740 Rattus
norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1						
mRNA, com						
gb_om:BOVPHOS	+	2798.00	4080.58	6.3e-219	1900	! L18966 Bos taurus
pyruvate dehydrogenase phosphatase mRNA, complete cds.						
11/1993						
gb_pat:AX180883	+	2792.00	4072.81	1.7e-218	1725	! AX180883 Sequence 10
from Patent WO0146394.	8/2001					
gb_pr:AF155661	+	2792.00	4068.67	2.9e-218	2555	! AF155661 Homo sapiens
pyruvate dehydrogenase (PDH) mRNA, complete cds.						
5/2000						
gb_ro:AF062741	+	1322.50	1920.38	1.3e-98	1750	! AF062741 Rattus
norvegicus pyruvate dehydrogenase phosphatase isoenzyme 2						
mRNA, com						

gb\_pat:AX287088 + 1321.50 1917.91 1.8e-98 1924 ! AX287088 Sequence 8  
from Patent WO0181590. 11/2001  
gb\_pr:AB037769 + 1321.50 1910.65 4.6e-98 3830 ! AB037769 Homo sapiens  
mRNA for KIAA1348 protein, partial cds. 3/2000  
gb\_pr:AC027131 + 1321.50 1868.62 1.0e-95 206102 ! AC027131 Homo  
sapiens chromosome 16 clone RP11-317I8, complete sequence. 2/2002  
gb\_ov:AF294839 + 1290.50 1874.67 4.6e-96 1567 ! AF294839 Danio rerio  
putative pyruvate dehydrogenase phosphatase isoenzyme 2 (pdp2)  
gb\_htg:AC101372 + 950.00 1336.41 4.4e-66 66671 ! AC101372 Mus musculus  
clone RP23-117E3, LOW-PASS SEQUENCE SAMPLING. 11/2001  
gb\_in:AY060985 + 838.50 1210.37 4.7e-59 1948 ! AY060985 Drosophila  
melanogaster GM14286 full length cDNA. 11/2001  
gb\_htg:AC101372 - 829.00 1159.19 3.3e-56 66671 ! AC101372 Mus musculus  
clone RP23-117E3, LOW-PASS SEQUENCE SAMPLING. 11/2001  
gb\_pr:AK022057 + 814.00 1171.45 6.9e-57 2598 ! AK022057 Homo sapiens  
cDNA FLJ11995 fis, clone HEMBB1001443, highly similar to Rattus  
gb\_htg:AC014483 + 782.00 1098.14 8.3e-53 31855 ! AC014483 Drosophila  
melanogaster, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in ordered pieces  
gb\_htg:AC104606 - 782.00 1079.70 8.9e-52 183175 ! AC104606 Drosophila  
melanogaster clone RP98-26L11, WORKING DRAFT SEQUENCE, 9 unorde  
gb\_in:AE003441 - 782.00 1075.03 1.6e-51 285272 ! AE003441 Drosophila  
melanogaster genomic scaffold 142000013386054 section 25 of 35,  
gb\_pr:AC009084 + 743.50 1023.27 1.2e-48 183865 ! AC009084 Homo  
sapiens chromosome 16 clone RP11-361L15, complete sequence. 2/2002  
gb\_htg:AC096087 - 673.50 928.09 2.5e-43 91605 ! AC096087 Rattus  
norvegicus clone CH230-14F3, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 45 uno  
gb\_in:AC006834 + 561.00 768.87 1.8e-34 54126 ! AC006834  
Caenorhabditis elegans cosmid ZK973, complete sequence. 10/2001  
gb\_htg:AC101398 - 555.50 758.69 6.7e-34 66199 ! AC101398 Mus musculus  
clone RP23-119N1, LOW-PASS SEQUENCE SAMPLING. 11/2001  
gb\_pl:NCB17C10 - 493.50 667.53 8.0e-29 68484 ! AL355926 Neurospora  
crassa DNA linkage group II BAC clone B17C10. 10/2001  
gb\_pl:SPAC10F6 - 457.50 620.97 3.2e-26 38139 ! AL009197 S.pombe  
chromosome I cosmid c10F6. 9/1999  
gb\_pl:SCYOR090C - 435.00 617.03 5.2e-26 2435 ! Z74998 S.cerevisiae  
chromosome XV reading frame ORF YOR090c. 8/1997  
gb\_pl:SC130KBXV - 435.00 575.12 1.1e-23 129528 ! X94335 S.cerevisiae  
130kb DNA fragment from chromosome XV. 7/1997  
gb\_pl:ATF9G14 + 300.50 380.37 8.0e-13 104769 ! AL162973 Arabidopsis  
thaliana DNA chromosome 5, BAC clone F9G14 (ESSA project). 4/2  
gb\_pl:AY062454 + 297.00 417.52 6.8e-15 1902 ! AY062454 Arabidopsis  
thaliana putative protein phosphatase-2c (At4g38520; F20M13.80  
gb\_pl:ATF20M13 - 292.50 370.03 3.0e-12 91938 ! AL035540 Arabidopsis  
thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project). 2/  
gb\_pl:ATF22I13 - 292.50 369.82 3.1e-12 93760 ! AL035539 Arabidopsis  
thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project). 8/  
gb\_pl:AC069558 + 292.50 368.36 3.7e-12 107740 ! AC069558 Genomic  
Sequence For Arabidopsis thaliana Clone T5G13 From Chromosome IV,  
gb\_pl:ATCHRIV89 - 292.50 361.84 8.6e-12 199789 ! AL161593 Arabidopsis  
thaliana DNA chromosome 4, contig fragment No. 89. 3/2000  
gb\_pl:AY050805 + 290.00 408.69 2.1e-14 1662 ! AY050805 Arabidopsis  
thaliana putative phosphatase 2C (F26O13.10/AT3g51370) mRNA, c  
gb\_pl:ATH302053 + 283.50 398.23 8.0e-14 1816 ! AJ302053 Arabidopsis  
thaliana PP2C6 gene for Ser/Thr protein phosphatase 2C, exons  
gb\_pl:ATT15C9 - 283.50 357.72 1.5e-11 84601 ! AL132970 Arabidopsis  
thaliana DNA chromosome 3, BAC clone T15C9. 4/2000

gb\_pl:AP002044 - 274.00 358.40 1.3e-11 21200 ! AP002044 *Arabidopsis thaliana* genomic DNA, chromosome 3, P1 clone: MMF12. 7/2000  
gb\_pl:AC069474 + 274.00 341.45 1.2e-10 105768 ! AC069474 *Arabidopsis thaliana* chromosome 3 BAC T2E22 genomic sequence, complete seq  
gb\_pl:FSY277744 + 272.00 380.38 7.9e-13 1999 ! AJ277744 *Fagus sylvatica* mRNA for ABA and calcium induced protein phosphatase 2C (P  
gb\_pl:AF079355 + 268.00 379.18 9.3e-13 1285 ! AF079355  
*Mesembryanthemum crystallinum* protein phosphatase-2c (PP2C) mRNA, partial  
gb\_pl:AY062587 + 266.50 374.10 1.8e-12 1689 ! AY062587 *Arabidopsis thaliana* protein phosphatase 2C-like protein (At5g66080; K2A18  
gb\_pl:AF097667 + 260.00 362.79 7.6e-12 2001 ! AF097667  
*Mesembryanthemum crystallinum* protein phosphatase 2C homolog (PP2C) mRNA,

Date: Aug 17, 2002 10:23 AM

About: Results were produced by the GenCore software, version 4.5,  
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Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlh
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Q=/cgn2_1/USPTO_spool/US09801267/runat_15082002_100803_5457/app_query.fasta_1.60
1
-DB=N_Geneseq_032802 -QFMT=fastap -SUFFIX=rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09801267@CGN1_1_184 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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Search information block:

Query: US-09-801-267-2  
Query length: 537  
Database: N\_Geneseq\_032802;\*  
Database sequences: 1736436  
Database length: 858457221  
Search time (sec): 197.420000

score\_list:

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/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT	AAD23607	+	2854.00	5285.72	4.5e-286	2634 ! Human protein phosphatase-4 (PP-4) DNA. Homo sapiens.
AAD23607;						
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT	AAD15455	+	2854.00	5284.86	5.1e-286	2838 ! Human 26583 serine/threonine phosphatase cDNA. Homo sapiens.
AAD15455;						
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT	AAI64180	+	2825.00	5236.20	2.6e-283	1779 ! Human pyruvate dehydrogenase phosphatase encoding cDNA. Homo sapiens. AAI64180;
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT	AAD09500	+	2792.00	5175.00	6.7e-280	1725 ! Human SGP040 phosphatase polypeptide encoding DNA. Homo sapiens. AAD09500;
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT	AAC91346	+	2723.00	5044.96	1.2e-272	1935 ! Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 46. Homo sapiens
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT	AAS31175	+	2367.50	4372.14	3.5e-235	4466 ! Human diagnostic and therapeutic polynucleotide (DITHP) #190. Homo sapiens. AAS31
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT	AAD23606	+	1321.50	2430.88	4.7e-127	1924 ! Human protein phosphatase-3 (PP-3) DNA. Homo sapiens.
AAD23606;						
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT	AAC75877	+	979.00	1803.61	4.1e-92	711 ! Human ORFX ORF1432 polynucleotide sequence SEQ ID NO:2863. Homo sapiens. AAC75877

/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABL04745 + 838.50 1531.50  
5.9e-77 1686 ! Drosophila melanogaster expressed polynucleotide SEQ ID NO  
8717. Drosophila melano  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAH04418 + 814.00 1497.03  
4.9e-75 642 ! Human cDNA clone (5'-primer) SEQ ID NO:1253. Homo sapiens.  
AAH04418;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAH17300 + 814.00 1480.78  
3.9e-74 2598 ! Human cDNA sequence SEQ ID NO:16701. Homo sapiens. AAH17300;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAS31351 + 791.00 1455.72  
9.8e-73 560 ! Human cDNA encoding a novel extracellular matrix protein, Seq  
ID No 165. Homo sapi  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABL04744 + 782.00 1414.99  
1.8e-70 4389 ! Drosophila melanogaster expressed polynucleotide SEQ ID NO  
8714. Drosophila melano  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAS31456 + 639.00 1173.97  
4.8e-57 481 ! Human cDNA encoding a novel extracellular matrix protein, Seq  
ID No 270. Homo sapi  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAL13615 - 616.00 1133.63  
8.5e-55 386 ! Human breast cancer expressed polynucleotide 6072. Homo  
sapiens. AAL13615;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAL13831 - 607.00 1117.27  
6.9e-54 372 ! Human breast cancer expressed polynucleotide 6288. Homo  
sapiens. AAL13831;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAL22484 - 596.00 1097.40  
8.9e-53 352 ! Human breast cancer expressed polynucleotide 14941. Homo  
sapiens. AAL22484;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAL22485 - 596.00 1097.40  
8.9e-53 352 ! Human breast cancer expressed polynucleotide 14942. Homo  
sapiens. AAL22485;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAL22697 - 592.00 1089.93  
2.3e-52 352 ! Human breast cancer expressed polynucleotide 15154. Homo  
sapiens. AAL22697;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAL13616 - 528.00 971.81  
8.8e-46 316 ! Human breast cancer expressed polynucleotide 6073. Homo  
sapiens. AAL13616;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABL04756 + 415.50 730.06  
2.6e-32 4915 ! Drosophila melanogaster expressed polynucleotide SEQ ID NO  
8750. Drosophila melano  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK52310 + 364.50 649.52  
7.9e-28 1402 ! Human polynucleotide SEQ ID NO 855. Homo sapiens. AAK52310;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK53294 + 364.50 649.47  
7.9e-28 1408 ! Human polynucleotide SEQ ID NO 2823. Homo sapiens. AAK53294;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAI94857 + 362.50 652.68  
5.2e-28 775 ! Human neuroblastoma expressed polynucleotide SEQ ID NO 932.  
Homo sapiens. AAI94857;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAF74203 + 296.00 518.80  
1.5e-20 1806 ! DNA encoding environmental stress tolerant protein SEQ ID 33.  
Avicennia marina. AA  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAF11932 + 295.50 521.82  
1.0e-20 1286 ! Aspergillus oryzae EST SEQ ID NO:4455. Aspergillus oryzae.  
AAF11932;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC44904 + 274.00 480.55  
2.0e-18 1422 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 44567.  
Arabidopsis thaliana. AAC44904  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC41862 + 268.50 467.76  
1.0e-17 1767 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 33410.  
Arabidopsis thaliana. AAC41862

/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC36215 + 266.50 464.57  
1.6e-17 1687 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 12968.  
Arabidopsis thaliana. AAC3621  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC46251 + 258.50 451.77  
8.1e-17 1406 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 49455.  
Arabidopsis thaliana. AAC4625  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC40305 + 258.50 451.74  
8.2e-17 1409 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 27828.  
Arabidopsis thaliana. AAC4030  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC47492 + 251.00 439.39  
4.0e-16 1224 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 54018.  
Arabidopsis thaliana. AAC4749  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC36491 + 247.00 425.05  
2.5e-15 2212 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 14006.  
Arabidopsis thaliana. AAC3649  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC47731 + 243.00 422.42  
3.5e-15 1460 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 54907.  
Arabidopsis thaliana. AAC4773  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC36341 + 240.50 417.85  
6.3e-15 1448 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 13444.  
Arabidopsis thaliana. AAC3634  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC41911 + 239.00 412.20  
1.3e-14 1851 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 33593.  
Arabidopsis thaliana. AAC4191  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC39393 + 238.00 410.85  
1.5e-14 1770 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 24465.  
Arabidopsis thaliana. AAC3939  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC49864 + 238.00 410.35  
1.6e-14 1848 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 62724.  
Arabidopsis thaliana. AAC4986  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAH26935 + 236.50 407.71  
2.3e-14 1824 ! Trichoderma reesei Ptc2, involved in unfolded protein  
response. Trichoderma reesei  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:AAD24598 + 236.50 407.71  
2.3e-14 1824 ! Trichoderma reesei ptc2 cDNA. Trichoderma reesei. AAD24598;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1993.DAT:AAQ60128 - 228.50 409.97  
1.7e-14 416 ! Human brain Expressed Sequence Tag EST02115. Homo sapiens.  
AAQ60128;  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC37530 + 221.00 383.73  
5.0e-13 1193 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 17721.  
Arabidopsis thaliana. AAC3753  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABL25549 + 217.00 369.77  
3.0e-12 2087 ! Drosophila melanogaster genomic polynucleotide SEQ ID NO  
28120. Drosophila melanog  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC35563 + 213.50 367.41  
4.1e-12 1458 ! Arabidopsis thaliana DNA fragment SEQ ID NO: 10636.  
Arabidopsis thaliana. AAC3556  
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAI57925 + 209.00 359.75  
1.1e-11 1369 ! Human polynucleotide SEQ ID NO 128. Homo sapiens. AAI57925;

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:AAD23607

Date: Aug 17, 2002 10:20 AM

About: Results were produced by the GenCore software, version 4.5,  
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Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09801267/runat_15082002_100802_5431/app_query.fasta_1.60
1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09801267 @CGN1_1_52 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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Search information block:

Query: US-09-801-267-2

Query length: 537

Database: Issued\_Patents\_NA:\*

Database sequences: 383533

Database length: 122816752

Search time (sec): 49.460000

score\_list:

Sequence	Strd	Orig	ZScore	EScore	Len	! Documentation	..
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-013-881-10	+	209.00	390.21	4.8e-14	1403	! Sequence 10, Application US/09013881	
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-935-855-19	+	176.00	318.66	4.6e-10	1890	! Sequence 19, Application US/08935855	
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-822-701-1	+	174.00	315.01	7.4e-10	1824	! Sequence 1, Application US/08822701	
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-935-855-1	+	174.00	315.01	7.4e-10	1824	! Sequence 1, Application US/08935855	
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-935-855-21	+	174.00	313.31	9.2e-10	2081	! Sequence 21, Application US/08935855	
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-873-093-2	+	169.50	302.97	3.5e-09	2268	! Sequence 2, Application US/08873093	
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-752-891-5	+	154.00	275.98	1.1e-07	1560	! Sequence 5, Application US/08752891	
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-144-178-5	+	154.00	275.98	1.1e-07	1560	! Sequence 5, Application US/09144178	
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-406-854-5	+	154.00	275.98	1.1e-07	1560	! Sequence 5, Application US/09406854	
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-752-891-1	+	148.00	263.67	5.3e-07	1560	! Sequence 1, Application US/08752891	
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4403765 ! Sequence 2, Application US/09103840A  
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3890 ! Sequence 1, Application US/08445474

Date: Aug 17, 2002 9:44 AM

About: Results were produced by the GenCore software, version 4.5,  
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Command line parameters:

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-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pdf -NORM=ext -HEAPSIZE=500
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Search information block:

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Query length: 537  
Database: EST:\*

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Search time (sec): 1595.140000

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full-length enriched, adult male diencephalon Mus musculus						
gb_est1:AV705571	+	961.00	1802.39	3.8e-91	631	! AV705571 AV705571 ADB
Homo sapiens cDNA clone ADBCFG09 5', mRNA sequence. 10/2000						
gb_est1:AV706533	+	961.00	1802.05	4.0e-91	649	! AV706533 AV706533 ADB
Homo sapiens cDNA clone ADBDVF06 5', mRNA sequence. 10/2000						
gb_est1:AI593115	-	901.00	1690.55	6.4e-85	533	! AI593115 vr31a07.y1
Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:11						
gb_est1:BB617574	+	878.00	1644.71	2.3e-82	640	! BB617574 BB617574 RIKEN
full-length enriched, adult male xiphoid cartilage Mus musc						
gb_est1:AW060691	+	861.00	1613.82	1.2e-80	571	! AW060691 UI-M-BH1-anl-
e-09-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-a						
gb_est2:BG038714	-	850.00	1593.55	1.6e-79	543	! BG038714 dd93f05.x1
Wellcome CRC pcDNA1 egg Xenopus laevis cDNA clone IMAGE:3431937						
gb_est1:AA637163	-	834.00	1563.66	7.5e-78	522	! AA637163 vr31a07.r1
Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:11						
gb_est1:BB623274	+	818.00	1530.90	5.0e-76	637	! BB623274 BB623274 RIKEN
full-length enriched, 12 days embryo male wolffian duct Mus						
gb_est1:AU120803	+	814.00	1523.22	1.3e-75	642	! AU120803 AU120803
HEMBB1 Homo sapiens cDNA clone HEMBB1001443 5', mRNA sequence. 10						
gb_est1:AV710801	+	813.00	1519.86	2.1e-75	725	! AV710801 AV710801 Cu
Homo sapiens cDNA clone CuAARG06 5', mRNA sequence. 10/2000						
gb_est2:BI460642	+	767.00	1433.19	1.4e-70	688	! BI460642 603201289F1
NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266870 5', mRNA sequ						

gb\_est2:BG088579 + 760.00 1421.76 6.0e-70 590 ! BG088579 H3155A02-5 NIA  
Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3155A02 5  
gb\_est2:BG348421 + 752.50 1409.34 3.0e-69 507 ! BG348421 dd93f05.y1  
Wellcome CRC pcDNA1 egg Xenopus laevis cDNA clone IMAGE:3431937  
gb\_est2:BG720546 + 707.00 1320.82 2.5e-64 608 ! BG720546 602691803F1  
NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4824168 5', mRNA sequ  
gb\_est1:BB611000 + 694.00 1296.65 5.6e-63 583 ! BB611000 BB611000 RIKEN  
full-length enriched, 11 days embryo Mus musculus cDNA clon  
gb\_est2:BG795101 + 677.00 1267.03 2.5e-61 468 ! BG795101 UTSW\_SM29G5  
UTSW Adult Mouse Skeletal Muscle Library Mus musculus cDNA clo  
gb\_est1:AI721530 - 675.50 1258.15 7.8e-61 773 ! AI721530 fc28g12.x1  
Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3722758  
gb\_est2:BG796457 + 674.00 1261.49 5.1e-61 462 ! BG796457 UTSW\_SM43G5  
UTSW Adult Mouse Skeletal Muscle Library Mus musculus cDNA clo  
gb\_est1:AI505570 + 669.00 1251.82 1.8e-60 469 ! AI505570 vr31a07.x1  
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gb\_est2:H09827 + 642.00 1200.33 1.3e-57 479 ! H09827 ym01a02.r1  
Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:46240 5' s  
gb\_est2:BI876371 + 633.00 1181.14 1.5e-56 571 ! BI876371 f171f05.y1  
Sugano Kawakami zebrafish DRA Danio rerio cDNA clone 3819393 5'  
gb\_est2:H10695 + 629.00 1176.60 2.7e-56 443 ! H10695 ym07h07.r1  
Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:47378 5' s  
gb\_est1:BB862687 + 596.00 1113.42 9.0e-53 464 ! BB862687 BB862687 RIKEN  
full-length enriched, colon RCB-0549 Cle-H3 cDNA Mus muscul  
gb\_gss:CNS04VQJ - 584.50 1081.69 5.3e-51 1058 ! AL309412 Tetraodon  
nigroviridis genome survey sequence T3 end of clone 045L07 of li  
gb\_est1:AI024308 - 572.00 1070.49 2.2e-50 373 ! AI024308 ov67f02.x1  
Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1642395 3' simi  
gb\_gss:AG183421 + 561.50 1043.66 6.9e-49 663 ! AG183421 Pan  
troglodytes DNA, clone: RP43-056O10.T7, genomic survey sequence. 1/200  
gb\_est1:BB857598 + 554.00 1033.51 2.5e-48 472 ! BB857598 BB857598 RIKEN  
full-length enriched, B16 F10Y cells Mus musculus cDNA clon  
gb\_est1:BE161595 - 550.50 1028.82 4.6e-48 401 ! BE161595 MR3-HT0446-  
260300-102-e12 HT0446 Homo sapiens cDNA, mRNA sequence. 6/2000  
gb\_est2:F05984 + 550.00 1030.59 3.7e-48 320 ! F05984 HSCOTA041  
normalized infant brain cDNA Homo sapiens cDNA clone c-0ta04, mRNA  
gb\_est1:AW520836 + 550.00 1026.60 6.2e-48 446 ! AW520836 UI-R-BJ0p-age-  
a-10-0-UI.s1 UI-R-BJ0p Rattus norvegicus cDNA clone UI-R-BJ0  
gb\_est1:AA891075 + 548.00 1026.75 6.1e-48 321 ! AA891075 EST194878  
Normalized rat heart, Bento Soares Rattus sp. cDNA clone RHEAO68  
gb\_est2:BF798554 + 539.00 1008.03 6.7e-47 368 ! BF798554 CM0-CI0060-  
031000-585-d11 CI0060 Homo sapiens cDNA, mRNA sequence. 1/2001  
gb\_est1:AU169045 - 537.50 1000.44 1.8e-46 546 ! AU169045 AU169045 ol-  
br-ad cDNA Oryzias latipes cDNA clone br4073, mRNA sequence. 1  
gb\_est1:BB860561 + 537.00 1001.48 1.6e-46 463 ! BB860561 BB860561 RIKEN  
full-length enriched, pooled cell lines Mus musculus cDNA c  
gb\_est1:BE103025 + 528.00 985.80 1.2e-45 412 ! BE103025 UI-R-BT1-aqr-  
e-01-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-a  
gb\_est2:BM262823 + 519.50 965.58 1.5e-44 579 ! BM262823 dai98h04.y1  
NICHD XGC Ovl Xenopus laevis cDNA clone IMAGE:5048671 5' simil  
gb\_est1:AI353989 + 517.50 965.93 1.5e-44 410 ! AI353989 zeh1250.seq.F  
Zebrafish Embryonic Heart cDNA Library Danio rerio cDNA 5',  
gb\_est2:BI884813 + 507.00 941.94 3.2e-43 575 ! BI884813 fo69f03.y1  
zebrafish gridded kidney Danio rerio cDNA clone 4725269 5' simil  
gb\_est1:BE095603 + 498.00 929.47 1.6e-42 392 ! BE095603 UI-R-B01-apo-  
a-03-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone UI-R-B01-a

gb\_gss:CNS02Q6Q + 491.50 905.70 3.4e-41 1015 ! AL208907 Tetraodon  
nigroviridis genome survey sequence PUC-Ori end of clone 157A02  
gb\_est1:AW606530 + 489.00 915.32 9.8e-42 307 ! AW606530 MR2-HT0380-  
290100-103-b11 HT0380 Homo sapiens cDNA, mRNA sequence. 3/2000  
gb\_est1:AU177305 + 486.50 903.02 4.7e-41 576 ! AU177305 AU177305  
Sugano-Kawakami 5' end enriched cDNA library (OLa) from HNI Oryzi  
gb\_est2:BM082541 + 484.00 898.21 8.8e-41 579 ! BM082541 fu22f05.y1  
Campbell zebrafish ovary Danio rerio cDNA clone 5306240 5' simi  
gb\_est2:BG702490 + 463.50 856.61 1.8e-38 725 ! BG702490 602684557F1  
NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:4816814 5', mRNA sequ

# SEQ ID NO 3

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 07:16:23 ; Search time 5492.57 Seconds  
(without alignments)  
6137.865 Million cell updates/sec

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Perfect score: 1611  
Sequence: 1 atgccagcaccaactcaact.....ggcgtatcaaaaccaagaa 1611

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pat:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_sts:

28: em\_un:\*
   
 29: em\_vi:\*
   
 30: em\_htg\_hum:\*
   
 31: em\_htg\_inv:\*
   
 32: em\_htg\_other:\*
   
 33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result	Query					Description
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3	1611	100.0	2838	6	AX249742	AX249742 Sequence
4	1611	100.0	250681	9	AP004282	AP004282 Homo sapi
5	1609.4	99.9	2495	9	AK057079	AK057079 Homo sapi
6	1583.2	98.3	1725	6	AX180883	AX180883 Sequence
7	1583.2	98.3	2555	9	AF155661	AF155661 Homo sapi
8	1574.2	97.7	1779	6	AX277696	AX277696 Sequence
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10	1409.4	87.5	2295	10	AF062740	AF062740 Rattus no
11	495.2	30.7	66671	2	AC101372	AC101372 Mus muscu
12	465.4	28.9	2598	9	AK022057	AK022057 Homo sapi
13	425.2	26.4	1750	10	AF062741	AF062741 Rattus no
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15	404.2	25.1	1924	6	AX287088	AX287088 Sequence
16	404.2	25.1	3830	9	AB037769	AB037769 Homo sapi
17	404.2	25.1	206102	9	AC027131	AC027131 Homo sapi
18	364.6	22.6	1567	5	AF294839	AF294839 Danio rer
c 19	298.2	18.5	66199	2	AC101398	AC101398 Mus muscu
20	219.2	13.6	183865	9	AC009084	AC009084 Homo sapi
c 21	195.8	12.2	91605	2	AC096087	AC096087 Rattus no
22	135.4	8.4	1948	3	AY060985	AY060985 Drosophil
23	87.8	5.5	54126	3	AC006834	AC006834 Caenorhab
24	80.4	5.0	31855	2	AC014483	AC014483 Drosophil
c 25	80.4	5.0	183175	2	AC104606	AC104606 Drosophil
c 26	80.4	5.0	285272	3	AE003441	AE003441 Drosophil
c 27	52.6	3.3	125020	9	AF429315	AF429315 Homo sapi
c 28	52	3.2	68484	8	NCB17C10	AL355926 Neurospor
29	51.4	3.2	104769	8	ATF9G14	AL162973 Arabidops
30	51.2	3.2	2712	8	AY062496	AY062496 Arabidops
31	49.8	3.1	178023	8	AC025783	AC025783 Oryza sat
32	49.6	3.1	1309	8	AB079669	AB079669 Arabidops
c 33	48.4	3.0	2435	8	SCYOR090C	Z74998 S.cerevisia
c 34	48.4	3.0	129528	8	SC130KBXV	X94335 S.cerevisia
35	47.4	2.9	94349	8	ATF26013	AL133452 Arabidops
36	46.2	2.9	1662	8	AY050805	AY050805 Arabidops
37	45.6	2.8	2039	8	AY061752	AY061752 Arabidops
38	45.4	2.8	1999	8	FSY277744	AJ277744 Fagus syl
c 39	45.2	2.8	38139	8	SPAC10F6	AL009197 S.pombe c
c 40	43.2	2.7	7218	6	I66494	I66494 Sequence 14
41	42.8	2.7	1824	6	AX319337	AX319337 Sequence

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43	41.8	2.6	1950	10	S90449	S90449 protein pho
44	41.8	2.6	2562	10	RNO271834	AJ271834 Rattus no
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Title: US-09-801-267-3  
Perfect score: 1611  
Sequence: 1 atgccagcaccaactcaact.....ggcgtatcaaaccagaa 1611

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_032802:\*

1: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT:\*

2: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:\*

3: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:\*

4: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT:\*

5: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT:\*

6: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT:\*

7: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:\*

8: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT:\*

9: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:\*

10: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT:\*

11: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT:\*

12: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT:\*

13: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1992.DAT:\*

14: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT:\*

15: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT:\*

16: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT:\*

17: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT:\*

18: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:\*

19: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:\*

20: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:\*

21: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:\*

22: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:\*

23: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:\*

24: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1611	100.0	2634	24	AAD23607	Human protein phos
2	1611	100.0	2838	22	AAD15455	Human 26583 serine
3	1583.2	98.3	1725	22	AAD09500	Human SGP040 phosp

4	1574.2	97.7	1779	24	AAI64180	Human pyruvate deh
5	1533.8	95.2	1935	22	AAC91346	Human polynucleoti
6	1285.6	79.8	4466	22	AAS31175	Human diagnostic a
7	537	33.3	711	21	AAC75877	Human ORFX ORF1432
8	465.4	28.9	642	22	AAH04418	Human cDNA clone (
9	465.4	28.9	2598	22	AAH17300	Human cDNA sequenc
10	430	26.7	560	22	AAS31351	Human cDNA encodin
11	404.2	25.1	1924	24	AAD23606	Human protein phos
c 12	358.4	22.2	372	22	AAL13831	Human breast cance
c 13	358.4	22.2	386	22	AAL13615	Human breast cance
c 14	349.8	21.7	481	22	AAS31456	Human cDNA encodin
c 15	348.4	21.6	352	22	AAL22484	Human breast cance
c 16	348.4	21.6	352	22	AAL22485	Human breast cance
c 17	346.8	21.5	352	22	AAL22697	Human breast cance
c 18	310.4	19.3	316	22	AAL13616	Human breast cance
19	268.4	16.7	775	22	AAI94857	Human neuroblastom
20	135.4	8.4	1686	23	ABL04745	Drosophila melanog
21	100.6	6.2	1402	22	AAK52310	Human polynucleoti
22	100.6	6.2	1408	22	AAK53294	Human polynucleoti
23	80.8	5.0	446	22	AAL14882	Human breast cance
24	80.4	5.0	4389	23	ABL04744	Drosophila melanog
25	73.2	4.5	794	22	AAL23742	Human breast cance
c 26	68	4.2	416	14	AAQ60128	Human brain Expres
27	54	3.4	4915	23	ABL04756	Drosophila melanog
28	51.2	3.2	1564	21	AAC38967	Arabidopsis thalia
29	51.2	3.2	2120	21	AAC36301	Arabidopsis thalia
30	45.6	2.8	1286	21	AAF11932	Aspergillus oryzae
31	42.8	2.7	1824	22	AAH26935	Trichoderma reesei
32	42.8	2.7	1824	24	AAD24598	Trichoderma reesei
33	42	2.6	1382	21	AAC32967	Arabidopsis thalia
34	41.4	2.6	1767	21	AAC41862	Arabidopsis thalia
35	39.6	2.5	552	20	AAX39627	Breast cancer asso
c 36	39.6	2.5	552	22	AAH09001	Human cDNA clone (
37	39.6	2.5	2268	23	ABL05227	Drosophila melanog
38	39.6	2.5	2270	20	AAX05715	Human protein phos
39	39.6	2.5	4504	23	ABL05226	Drosophila melanog
40	39.2	2.4	2543	21	AAF15879	Human prostate can
41	39.2	2.4	2543	21	AAZ97065	Human secreted pro
42	39	2.4	472	21	AAC21427	Human secreted pro
43	38	2.4	1422	21	AAC44904	Arabidopsis thalia
44	37.8	2.3	1206	21	AAC51886	Arabidopsis thalia
45	37.8	2.3	1409	21	AAC52147	Arabidopsis thalia

Title: US-09-801-267-3  
Perfect score: 1611  
Sequence: 1 atgccagcaccaactcaact.....ggcgtatcaaaaccaagaa 1611

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:/\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:/\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:/\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:/\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:/\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Query				Description
	Score	Match	Length	DB ID	
c 1	43.2	2.7	7218	1 US-08-232-463-14	Sequence 14, Appl
c 2	39.6	2.5	2268	2 US-08-873-093-2	Sequence 2, Appli
c 3	32.6	2.0	3495	4 US-08-827-962-17	Sequence 17, Appl
c 4	32.6	2.0	3650	3 US-08-837-635-5	Sequence 5, Appli
c 5	32.6	2.0	3650	3 US-08-837-635-7	Sequence 7, Appli
c 6	32.6	2.0	3650	4 US-08-827-962-16	Sequence 16, Appl
c 7	32.6	2.0	3650	4 US-08-803-346-2	Sequence 2, Appli
c 8	32	2.0	5058	4 US-08-934-386-8	Sequence 8, Appli
c 9	32	2.0	9361	4 US-08-934-386-7	Sequence 7, Appli
c 10	31.8	2.0	2107	4 US-08-235-836C-73	Sequence 73, Appl
c 11	31.8	2.0	3290	1 US-07-985-691-1	Sequence 1, Appli
c 12	31.8	2.0	3290	1 US-08-436-804-1	Sequence 1, Appli
c 13	31.8	2.0	3290	1 US-08-267-387-1	Sequence 1, Appli
c 14	31.8	2.0	6811	3 US-08-651-472-67	Sequence 67, Appl
c 15	31.8	2.0	6811	4 US-08-358-928-67	Sequence 67, Appl
c 16	31.6	2.0	162	2 US-08-469-537A-32	Sequence 32, Appl
c 17	31.6	2.0	3592	2 US-08-469-537A-100	Sequence 100, App
c 18	31.6	2.0	3919	1 US-08-301-722A-1	Sequence 1, Appli
c 19	31.4	1.9	3112	4 US-09-318-448-9	Sequence 9, Appli
c 20	31	1.9	1863	3 US-09-126-646-1	Sequence 1, Appli
c 21	31	1.9	2882	1 US-08-393-219-2	Sequence 2, Appli

22	30.8	1.9	906	1	US-08-100-874-1	Sequence 1, Appli
23	30.8	1.9	59065	4	US-09-813-817-3	Sequence 3, Appli
24	30.4	1.9	2573	3	US-08-714-918-17	Sequence 17, Appli
25	30.4	1.9	2573	3	US-08-714-918-64	Sequence 64, Appli
26	30.4	1.9	2573	4	US-09-265-315-17	Sequence 17, Appli
27	30.4	1.9	2573	4	US-09-265-315-64	Sequence 64, Appli
28	30.4	1.9	2573	4	US-09-265-315-17	Sequence 17, Appli
29	30.4	1.9	2573	4	US-09-265-315-64	Sequence 64, Appli
30	30.4	1.9	2573	4	US-09-266-417-17	Sequence 17, Appli
31	30.4	1.9	2573	4	US-09-266-417-64	Sequence 64, Appli
32	30.2	1.9	1991	4	US-08-235-836C-69	Sequence 69, Appli
33	30.2	1.9	1991	4	US-08-235-836C-77	Sequence 77, Appli
c 34	30.2	1.9	3284	6	5258288-3	Patent No. 5258288
35	30.2	1.9	6744	1	US-08-119-125A-2	Sequence 2, Appli
c 36	30	1.9	1801	4	US-08-669-304-30	Sequence 30, Appli
c 37	29.8	1.8	657	1	US-07-621-091G-2	Sequence 2, Appli
c 38	29.8	1.8	657	2	US-08-399-889-2	Sequence 2, Appli
c 39	29.8	1.8	657	3	US-09-167-364-2	Sequence 2, Appli
c 40	29.8	1.8	657	4	US-09-439-897-3	Sequence 3, Appli
41	29.8	1.8	773	2	US-08-970-133-4	Sequence 4, Appli
42	29.8	1.8	773	4	US-09-294-545-4	Sequence 4, Appli
43	29.6	1.8	247	4	US-09-344-888A-24	Sequence 24, Appli
c 44	29.6	1.8	626	4	US-09-385-982-199	Sequence 199, App
c 45	29.6	1.8	656	4	US-09-385-982-333	Sequence 333, App

Perfect score: 1611  
Sequence: 1 atgccagcaccaactcaact.....ggcgtatcaaaccagaa 1611

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_gss:\*

13: em\_gss\_hum:\*

14: em\_gss\_inv:\*

15: em\_gss\_pln:\*

16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	545	33.8	631	9	AV705571	AV705571 AV705571
2	545	33.8	649	9	AV706533	AV706533 AV706533
3	542	33.6	651	9	BB625845	BB625845 BB625845
4	465.4	28.9	642	9	AU120803	AU120803 AU120803
5	460.4	28.6	725	9	AV710801	AV710801 AV710801
c 6	455	28.2	533	9	AI593115	AI593115 vr31a07.y
7	438.2	27.2	640	9	BB617574	BB617574 BB617574
8	429.4	26.7	571	9	AW060691	AW060691 UI-M-BH1-
9	416	25.8	637	9	BB623274	BB623274 BB623274
c 10	415	25.8	522	9	AA637163	AA637163 vr31a07.r
11	414	25.7	688	10	BI460642	BI460642 603201289
12	388.4	24.1	608	10	BG720546	BG720546 602691803
13	386.2	24.0	590	10	BG088579	BG088579 H3155A02-

14	364.2	22.6	479	10	H09827	H09827 ym01a02.rl
15	359	22.3	443	10	H10695	H10695 ym07h07.rl
16	345.4	21.4	468	10	BG795101	BG795101 UTSW_SM29
17	343.6	21.3	462	10	BG796457	BG796457 UTSW_SM43
18	337.8	21.0	583	9	BB611000	BB611000 BB611000
c 19	335.8	20.8	543	10	BG038714	BG038714 dd93f05.x
c 20	328.6	20.4	401	9	BE161595	BE161595 MR3-HT044
21	327	20.3	469	9	AI505570	AI505570 vr31a07.x
22	326.4	20.3	368	10	BF798554	BF798554 CM0-CI006
23	320	19.9	320	10	F05984	F05984 HSC0TA041 n
c 24	300	18.6	373	9	AI024308	AI024308 ov67f02.x
25	289	17.9	307	9	AW606530	AW606530 MR2-HT038
26	287.8	17.9	464	9	BB862687	BB862687 BB862687
27	276.6	17.2	507	10	BG348421	BG348421 dd93f05.y
28	267.6	16.6	472	9	BB857598	BB857598 BB857598
29	266.6	16.5	446	9	AW520836	AW520836 UI-R-BJ0p
30	264.6	16.4	321	9	AA891075	AA891075 EST194878
31	258.2	16.0	412	9	BE103025	BE103025 UI-R-BT1-
32	257.2	16.0	463	9	BB860561	BB860561 BB860561
33	253.8	15.8	299	9	AW606531	AW606531 MR2-HT038
34	239.4	14.9	392	9	BE095603	BE095603 UI-R-BO1-
35	230	14.3	571	10	BI876371	BI876371 f171f05.y
36	228.8	14.2	725	10	BG702490	BG702490 602684557
37	224.4	13.9	252	9	AA765631	AA765631 oa08f01.s
38	218.8	13.6	286	9	AA374379	AA374379 EST86524
39	203.2	12.6	447	9	BB863307	BB863307 BB863307
c 40	202.4	12.6	546	9	AU169045	AU169045 AU169045
41	201	12.5	642	10	BG703862	BG703862 602686908
42	198.6	12.3	442	9	BB858560	BB858560 BB858560
c 43	192.2	11.9	773	9	AI721530	AI721530 fc28g12.x
44	190.2	11.8	575	10	BI884813	BI884813 fo69f03.y
45	182.8	11.3	579	10	BM262823	BM262823 dai98h04.